

SEQUENCE LISTING

<110> WILLIAMS, R. SANDERS
ROTHERMEL, BEVERLY

<120> METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
CALCINEURIN INTERACTING PROTEIN (MCIP)

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<140> UNKNOWN

<141> 2001-02-13

<150> 60/216,601

<151> 2000-07-07

<160> 27

<170> PatentIn Ver. 2.1

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Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr	
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D E B I T O R

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Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Met Glu Arg
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Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser His Pro Lys Ser Ala
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Ala Arg Ala Arg Ile Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys

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Lys Leu His Leu Ala Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser
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Pro Pro Ser Ser Pro Pro Val Gly Trp Lys Pro Ile Ser Asp Ala Thr
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Pro Val Leu Asn Tyr Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro
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Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Phe Ser Ala
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Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
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Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
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Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
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Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu Glu Met Glu Arg Met
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Pro Ile His Leu Ser
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35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Phe Ser Ala
50 55 60

Ala Asp Ala Arg Leu Gln Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn

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0978293.021301

115 120 125
Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
130 135 140
Glu Leu His Ala Ala Thr Asp Thr Thr Pro Ser Val Val Val His Val
145 150 155 160
Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu Glu Met Glu Arg Met
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Arg Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr Thr
180 185 190
Pro Ile His Leu Ser
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ctggaagctc ttcccttcac tcccaactct gaggttgccct aactctttat taaaaattca 180
gaagggggaa tgccagcccc tagc atg gac tgt gat gtt tcc act ctg gtt 231
Met Asp Cys Asp Val Ser Thr Leu Val
1 5
gcc tgt gtg gtg gat gtc gag gtc ttt acc aat cag gag gtt aag gaa 279
Ala Cys Val Val Asp Val Glu Val Phe Thr Asn Gln Glu Val Lys Glu
10 15 20 25
aaa ttt ggg gga ctg ttt cgg act tat gat gac tgt gtg acg ttc cag 327
Lys Phe Gly Gly Leu Phe Arg Thr Tyr Asp Asp Cys Val Thr Phe Gln
30 35 40
cta ttt aag agt ttc aga cgt gtc cgt ata aac ttc agc aat cct aaa 375
Leu Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Asn Pro Lys

45

50

55

tct gca gcc cga gct agg ata gag ctt cat gaa acc caa ttc aga ggg 423
Ser Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Gln Phe Arg Gly
60 65 70

aaa aaa tta aag ctc tac ttt gca cag gtt cag act cca gag aca gat 471
Lys Lys Leu Lys Leu Tyr Phe Ala Gln Val Gln Thr Pro Glu Thr Asp
75 80 85

gga gac aaa ctg cac ttg gct cca ccc cag cct gcc aaa cag ttt ctc 519
Gly Asp Lys Leu His Leu Ala Pro Pro Gln Pro Ala Lys Gln Phe Leu
90 95 100 105

atc tcg ccc cct tcc tcc cca cct gtt agc tgg cag ccc atc aac gat 567
Ile Ser Pro Pro Ser Ser Pro Pro Val Ser Trp Gln Pro Ile Asn Asp
110 115 120

gcc acg cca gtc ctc aac tat gac ctc ctc tat gct gtg gcc aaa cta 615
Ala Thr Pro Val Leu Asn Tyr Asp Leu Leu Tyr Ala Val Ala Lys Leu
125 130 135

gga cca gga gag aag tat gag ctc cat gca ggg act gag tcc acc cca 663
Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro
140 145 150

agt gtc gtc gtg cac gtg tgc gac agt gac ata gag gaa gaa gag gac 711
Ser Val Val Val His Val Cys Asp Ser Asp Ile Glu Glu Glu Glu Asp
155 160 165

cca aag act tcc cca aag cca aaa atc atc caa act cgg cgt cct ggc 759
Pro Lys Thr Ser Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Gly
170 175 180 185

ctg cca ccc tcc gtg tcc aac tgagctgcct gctccttctc gataatagcc 810
Leu Pro Pro Ser Val Ser Asn
190

gtctcctctt tatcatgctt tttccccctg ttgtttgtca aaaaaaattg ccttttaaatt 870

cctgggtgtt tggttggttg agattccttc ctgttatca agcctctcgg acaaaaagggc 930

taggaaaagg tgatatgtct cctgatcata tcatacccat taagtataac ccattattta 990

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<210> 18

<211> 192

<212> PRT

<213> Homo sapiens

<400> 18

Met Asp Cys Asp Val Ser Thr Leu Val Ala Cys Val Val Asp Val Glu
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Val Phe Thr Asn Gln Glu Val Lys Glu Lys Phe Gly Gly Leu Phe Arg
20 25 30

Thr Tyr Asp Asp Cys Val Thr Phe Gln Leu Phe Lys Ser Phe Arg Arg
35 40 45

Val Arg Ile Asn Phe Ser Asn Pro Lys Ser Ala Ala Arg Ala Arg Ile
50 55 60

Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys Leu Lys Leu Tyr Phe
65 70 75 80

Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp Lys Leu His Leu Ala
85 90 95

Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser Pro Pro Ser Ser Pro

Pro Val Ser Trp Gln Pro Ile Asn Asp Ala Thr Pro Val Leu Asn Tyr
 115 120 125
 Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro Gly Glu Lys Tyr Glu
 130 135 140
 Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys
 145 150 155 160
 Asp Ser Asp Ile Glu Glu Glu Glu Asp Pro Lys Thr Ser Pro Lys Pro
 165 170 175
 Lys Ile Ile Gln Thr Arg Arg Pro Gly Leu Pro Pro Ser Val Ser Asn
 180 185 190

<210> 19
 <211> 192
 <212> PRT
 <213> Homo sapiens

<400> 19
 Met Asp Cys Asp Val Ser Thr Leu Val Ala Cys Val Val Asp Val Glu
 1 5 10 15
 Val Phe Thr Asn Gln Glu Val Lys Glu Lys Phe Gly Gly Leu Phe Arg
 20 25 30
 Thr Tyr Asp Asp Cys Val Thr Phe Gln Leu Phe Lys Ser Phe Arg Arg
 35 40 45
 Val Arg Ile Asn Phe Ser Asn Pro Lys Ser Ala Ala Arg Ala Arg Ile
 50 55 60
 Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys Leu Lys Leu Tyr Phe
 65 70 75 80
 Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp Lys Leu His Leu Ala
 85 90 95
 Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser Pro Pro Ser Ser Pro
 100 105 110
 Pro Val Ser Trp Gln Pro Ile Asn Asp Ala Thr Pro Val Leu Asn Tyr
 115 120 125

Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro Gly Glu Lys Tyr Glu
 130 135 140

Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys
 145 150 155 160

Asp Ser Asp Ile Glu Glu Glu Asp Pro Lys Thr Ser Pro Lys Pro
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Lys Ile Ile Gln Thr Arg Arg Pro Gly Leu Pro Pro Ser Val Ser Asn
 180 185 190

<210> 20

<211> 828

<212> DNA

<213> Homo sapiens

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<222> (23)..(745)

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gat agc cag tca gat ctg tgt agc act gac caa gaa gag gaa gaa gag 100
 Asp Ser Gln Ser Asp Leu Cys Ser Thr Asp Gln Glu Glu Glu Glu Glu
 15 20 25

atg att ttt ggt gaa aat gaa gat gat ttg gat gag atg atg gat tta 148
 Met Ile Phe Gly Glu Asn Glu Asp Asp Leu Asp Glu Met Met Asp Leu
 30 35 40

agt gat ctg cct acc tca ctt ttt gct tgc agc gtc cat gaa gca gtg 196
 Ser Asp Leu Pro Thr Ser Leu Phe Ala Cys Ser Val His Glu Ala Val
 45 50 55

ttt gag gca cga gag cag aag gaa aga ttt gaa gca ctc ttc acc atc 244
 Phe Glu Ala Arg Glu Gln Lys Glu Arg Phe Glu Ala Leu Phe Thr Ile
 60 65 70

tat gat gac cag gtt act ttt cag ctg ttt aaa agc ttt aga aga gtc 292

Tyr	Asp	Asp	Gln	Val	Thr	Phe	Gln	Leu	Phe	Lys	Ser	Phe	Arg	Arg	Val	
75					80					85					90	
aga	ata	aat	ttc	agc	aaa	cct	gaa	gcg	gca	gca	aga	gcg	cga	ata	gaa	340
Arg	Ile	Asn	Phe	Ser	Lys	Pro	Glu	Ala	Ala	Ala	Arg	Ala	Arg	Ile	Glu	
				95				100						105		
ctc	cac	gaa	aca	gac	ttc	aat	ggg	cag	aag	cta	aag	cta	tat	ttt	gca	388
Leu	His	Glu	Thr	Asp	Phe	Asn	Gly	Gln	Lys	Leu	Lys	Leu	Tyr	Phe	Ala	
			110					115					120			
cag	gtg	cag	atg	tcc	ggc	gaa	gtg	cgg	gac	aag	tcc	tat	ctc	ctg	ccg	436
Gln	Val	Gln	Met	Ser	Gly	Glu	Val	Arg	Asp	Lys	Ser	Tyr	Leu	Leu	Pro	
		125					130					135				
ccc	cag	cct	gtc	aag	cag	ttc	ctc	atc	tcc	cct	cca	gcc	tct	ccc	cca	484
Pro	Gln	Pro	Val	Lys	Gln	Phe	Leu	Ile	Ser	Pro	Pro	Ala	Ser	Pro	Pro	
		140				145						150				
gtg	ggg	tgg	aag	cag	agc	gaa	gat	gcg	atg	cct	gtt	ata	aat	tat	gat	532
Val	Gly	Trp	Lys	Gln	Ser	Glu	Asp	Ala	Met	Pro	Val	Ile	Asn	Tyr	Asp	
155					160					165					170	
tta	ctc	tgt	gct	gtt	tcc	aaa	ttg	gga	cca	gga	gag	aaa	tat	gaa	ctt	580
Leu	Leu	Cys	Ala	Val	Ser	Lys	Leu	Gly	Pro	Gly	Glu	Lys	Tyr	Glu	Leu	
				175					180					185		
cac	gcg	gga	aca	gag	tcg	aca	ccc	agc	gtg	gtg	gtt	cat	gtc	tgt	gaa	628
His	Ala	Gly	Thr	Glu	Ser	Thr	Pro	Ser	Val	Val	Val	His	Val	Cys	Glu	
			190					195					200			
agt	gaa	act	gaa	gag	gaa	gaa	gag	aca	aaa	aac	ccc	aaa	cag	aaa	att	676
Ser	Glu	Thr	Glu	Glu	Glu	Glu	Glu	Thr	Lys	Asn	Pro	Lys	Gln	Lys	Ile	
		205					210					215				
gcc	cag	aca	agg	cgc	ccc	gac	cct	ccg	acc	gca	gcg	ttg	aat	gag	ccc	724
Ala	Gln	Thr	Arg	Arg	Pro	Asp	Pro	Pro	Thr	Ala	Ala	Leu	Asn	Glu	Pro	
		220				225					230					
cag	acc	ttt	gat	tgc	gcg	ctg	tgaggccctt	ggttgtggtg	cgaggcggt							775
Gln	Thr	Phe	Asp	Cys	Ala	Leu										
235					240											
gccctggtgg	gctctggcca	tggcgctctg	tgccctgcggc	cgatgcgttg	ctg											828

<210> 21
<211> 241

<212> PRT

<213> Homo sapiens

<400> 21

Met Leu Arg Asp Thr Met Lys Ser Trp Asn Asp Ser Gln Ser Asp Leu
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Cys Ser Thr Asp Gln Glu Glu Glu Glu Met Ile Phe Gly Glu Asn
20 25 30

Glu Asp Asp Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser
35 40 45

Leu Phe Ala Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln
50 55 60

Lys Glu Arg Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr
65 70 75 80

Phe Gln Leu Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys
85 90 95

Pro Glu Ala Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe
100 105 110

Asn Gly Gln Lys Leu Lys Leu Tyr Phe Ala Gln Val Gln Met Ser Gly
115 120 125

Glu Val Arg Asp Lys Ser Tyr Leu Leu Pro Pro Gln Pro Val Lys Gln
130 135 140

Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Ser
145 150 155 160

Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys Ala Val Ser
165 170 175

Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser
180 185 190

Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr Glu Glu Glu
195 200 205

Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr Arg Arg Pro
210 215 220

Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe Asp Cys Ala
225 230 235 240

Leu

<210> 22

<211> 241

<212> PRT

<213> Homo sapiens

<400> 22

Met Leu Arg Asp Thr Met Lys Ser Trp Asn Asp Ser Gln Ser Asp Leu
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Cys Ser Thr Asp Gln Glu Glu Glu Glu Met Ile Phe Gly Glu Asn
20 25 30

Glu Asp Asp Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser
35 40 45

Leu Phe Ala Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln
50 55 60

Lys Glu Arg Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr
65 70 75 80

Phe Gln Leu Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys
85 90 95

Pro Glu Ala Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe
100 105 110

Asn Gly Gln Lys Leu Lys Leu Tyr Phe Ala Gln Val Gln Met Ser Gly
115 120 125

Glu Val Arg Asp Lys Ser Tyr Leu Leu Pro Pro Gln Pro Val Lys Gln
130 135 140

Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Ser
145 150 155 160

Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys Ala Val Ser
165 170 175

Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser
180 185 190

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Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr Glu Glu Glu
 195 200 205

Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr Arg Arg Pro
 210 215 220

Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe Asp Cys Ala
 225 230 235 240

Leu

<210> 23
 <211> 720
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (2)..(637)

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ttg gat gag atg atg gat tta agt gat ctg cct acc tca ctt ttt gct 97
 Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser Leu Phe Ala
 20 25 30

tgc agc gtc cat gaa gca gtg ttt gag gca cga gag cag aag gaa aga 145
 Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln Lys Glu Arg
 35 40 45

ttt gaa gca ctc ttc acc atc tat gat gac cag gtt act ttt cag ctg 193
 Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr Phe Gln Leu
 50 55 60

ttt aaa agc ttt aga aga gtc aga ata aat ttc agc aaa cct gaa gcg 241
 Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys Pro Glu Ala
 65 70 75 80

gca gca aga gcg cga ata gaa ctc cac gaa aca gac ttc aat ggg cag 289
 Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe Asn Gly Gln
 85 90 95

aag cta aag cta tat ttt gca cag tcc tat ctc ctg ccg ccc cag cct 337

Lys Leu Lys Leu Tyr Phe Ala Gln Ser Tyr Leu Leu Pro Pro Gln Pro
 100 105 110

gtc aag cag ttc ctc atc tcc cct cca gcc tct ccc cca gtg ggg tgg 385
 Val Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp
 115 120 125

aag cag agc gaa gat gcg atg cct gtt ata aat tat gat tta ctc tgt 433
 Lys Gln Ser Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys
 130 135 140

gct gtt tcc aaa ttg gga cca gga gag aaa tat gaa ctt cac gcg gga 481
 Ala Val Ser Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly
 145 150 155 160

aca gag tcg aca ccc agc gtg gtg gtt cat gtc tgt gaa agt gaa act 529
 Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr
 165 170 175

gaa gag gaa gaa gag aca aaa aac ccc aaa cag aaa att gcc cag aca 577
 Glu Glu Glu Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr
 180 185 190

agg cgc ccc gac cct ccg acc gca gcg ttg aat gag ccc cag acc ttt 625
 Arg Arg Pro Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe
 195 200 205

gat tgc gcg ctg tgaggccctt gggtgtggtg cgaggcggct gccctggtgg 677
 Asp Cys Ala Leu
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gctctggcca tggcgctctg tgcctgcggc cgatgcgttg ctg 720

<210> 24

<211> 212

<212> PRT

<213> Homo sapiens

<400> 24

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Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser Leu Phe Ala
 20 25 30

Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln Lys Glu Arg
 35 40 45

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Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr Phe Gln Leu
50 55 60

Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys Pro Glu Ala
65 70 75 80

Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe Asn Gly Gln
85 90 95

Lys Leu Lys Leu Tyr Phe Ala Gln Ser Tyr Leu Leu Pro Pro Gln Pro
100 105 110

Val Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp
115 120 125

Lys Gln Ser Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys
130 135 140

Ala Val Ser Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly
145 150 155 160

Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr
165 170 175

Glu Glu Glu Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr
180 185 190

Arg Arg Pro Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe
195 200 205

Asp Cys Ala Leu
210

<210> 25

<211> 212

<212> PRT

<213> Homo sapiens

<400> 25

Asp Gln Glu Glu Glu Glu Met Ile Phe Gly Glu Asn Glu Asp Asp
1 5 10 15

Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser Leu Phe Ala
20 25 30

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 aattaacttt gcttggggag aatggaaaaa acagctgagg tttgcttcac agctgcttta 420
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 aacctggaaa ccaaagtccg ggtgacatac ttgatccctg gaatttcctg aaaacctcaa 660
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 acattttatt ggatgaatgt cccaattttc attgttatcc cacagtggaa tggagcaaac 840
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 ggggatatga aacacttcga tcattttcaa agcactactg aattcaggca aaggatacaa 960
 aaacactagc ctttgaaact gagcaatcta gcctttgaaa ctgagcaaag aagcattaac 1020
 ccatttatgc cagaggttg 1039

<210> 27

<211> 853

<212> DNA

<213> Homo sapiens

<400> 27

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 atgaaaatcc taggattgtt ttaggttctg tttgtccat tccactgtgg gatacaagta 180
 gaaattggga cattcatcca ataaaatgtc actggggaaa aaaattttta ctacacttca 240
 aaatgattcc tctttttgtc ctttaaaatt tttattgacc aagacagatt tcaaaatgtt 300
 ttctctaata ccccaaagtg aaactttgat tgagggtttc aggaaattcc agggatcaag 360
 tatgtcacc ggacttttgt ttccagggtt cccaaagtct tgaaatttcc ctacagtcta 420
 attgctgttt attgccacag accttcatcc tttttctttt gtaacatttt ccatcttaag 480
 aagggtcgtc ccattcggcc gaggagcgtg ttgtctgagt agctgaatgg aattactacg 540
 agtggaact atgctgcaag agaggttgat aaagcagctg tgaagcaaac ctcagctgtt 600
 ttttccattc tccccagca aagttaatta gcatagggaa aatgactaag gtgttgacgt 660
 cacctctttc cagtagaaac ttacactttg tccctgtcta cctgcaagca tgcaggactt 720
 gactcaggaa tttgctgtcc aaacaggatg ctgtggaagc tgcacttttt ttttccccag 780
 ggagtggggg ctggccctta ctgctttata agcaccagct caagaaggaa cctacagcct 840
 cttggaaagg aat 853

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